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(without alignments)
330.553 Million cell updates/sec
                                                                                                          January 16, 2003, 16:55:57; Search time 968.471 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                     nucleic scatch, using frame_pius_p2n model
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Ygapop 10.0 , Ygapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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24	Result No.	Score	Query Match	Length	DB	OH.	Description
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HKLTRDOWEDKIQVWHAEHRGMLKDSAMLEYI.KIAQDLEMYGINYFEIKNKKGTDIMI.
GVDALGINIYEKDDKLTPRIGFPWSEIRNISFNDKKFVIKPIDKKADDFVFYAPRIRI
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FGLOYVDNKGFPTWLKIDKKVSAQEVRKESPIQFKFPAKFYPEDVAEELIQDITGKLF
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                                                                                                                                                                                                                     Eukaryoia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Cetarliodactyla; Ruminantia; Pecora; Bovoidea; Bovidea; Bovidea; Bosidea; Bosid
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Turunen,O., Winqvist,R., Pakkanen,R., Grzeschik,K.H., Wahlstrom,T.
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Human placenta, cDNA to mKNA.
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/tissue_type-"brain"
152. .1897
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Draft entry and computer-readable sequence for [1] kindly submitted by O.Turunen, 31-AUG-1989.

Localion/Qualifiers
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Adb_xrei=13.40.21.7
/db_xrei="cD8:300-120-489"
/!ranslation="MDAFLEFAIQPNTTGKQLFDQVVKTIGLREVWYFGLHYVDNKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELYMRRRRPDT TEVQOMKAQAREEKHOKQLERQQLETEKKRRETVEREKEOMMREKE
ELMLRLQDYEEKTKKAERELSEQIQRAIQIJEEFRKRAGEEABRLEADUMAALRAKEEL
ERQAVDO I KSQEQIJAAELJAFYTAK I ALLEEARRRKEDEVEEWOHRAKEAGDDLVKTYE
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ELYCPPETAVLLGSYAVQAKFGDYNKEVHKSGYLSSEKLI PORVMDOHKLTRDOMEDR
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FAEKNERVQRQLVTLSSELSQARDENKPTHNDLTHNENMRQGRDKYKTLRQTRQGNTK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: Wo 0229103-A 3721 11-APR 2002;
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/db_xref="taxon.9466"
/note="EMBL/GenBank Accession No. X51521"
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                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-JAN 1990) Hunter T., The Salk institute, Molecular Biology and Virology Laboratory, 10616 North Torrey Pines Road, San Diego. CA 92138, USA
2. (Dases 1 to 3044)
Gould,K.L., Bretscher,A., Esch,F.S. and Hunter,T.
Sound, M.D., Markenson of the protein tyrosine kinase substrate, ezrin, reveals homology to band 4.1
EMHO J. 8 (13), 4133-4142 (1989)
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GVDALGENI YEKDDKLIPKI GEPWSEIRNI SPNDKREVI KPITKKADPEVEYAPRIPT
NKRILQLOWHELYMPRREPTI EWQMKAQAPRENIQKOLEBGALETEKRRETVE
REKEĞMMREKEELMI KIÇDE BEKI KRABKELSEÇI ÇKALULEBERK RAÇEBALKILADI
KMAALKARKEELERQYNO I KŞQĞQIAAELARYTAKI ALLEBARRKEDEVERWOHKAK
EQQDDI,VKT KEELHI,VMTAPPPPPPVEPVSEYYAKI ALLEBARRKEDEVERWOHKAK
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FCLHVVINKOFPTWORDELDKKVSAQIYPKENINGFREFAKFYLGEVALLIOL JOHGE
FLQVRBGILSCEIYCPPELAVLLIGSYAVQAKFÖDENKEVHKSGYLSSERLIPQRVMDQ
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
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ezrin, kinase substrate, microvilli protein
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/cell_line-"HeLa"
/clone_lib-"Okayama-Berg"
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/db_xre1-"GI:31283"
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information about the clone and the sequencing project is available
at http://www.mips.biochem.mpq.de/proj/cDNA/.
              linear PAL 28-JUN 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapions
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ottenwaelder,B., Obermaler,B., Mewes,H.W., Weil,B. and Wiemann,S.
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Ludes,M.J., Algate,F.A., Filing,S.P., Mannion,J., Renson,D.P.
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Research Center (DKF2); Email s.wiemannedkíz-heidelberg.de;
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Martinsried, GERMANY
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AX440476
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/db_xref-"taxon:9606"
3947 bp
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KLDKFVSAGEVPFENPLGFFFFARTYPFTVAELETIQNITARLFELGVEKSILESDETW
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WHAEHRGMILKDNAMILEYIK IAQDILEMYĞINYFEIKNKGFDIW HIGVRITIPGQMEDPLQV
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YMRRRK PDT I EVQQMKAQAREEKIIQKQLERQQLETEKKRRETVEREKEQMMREKEELM
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LVMTAPPPPPPVYEPVSYHVÖESLÖDEGAEPTGYSAELSSEGTKUDKNEEKRTTEAF
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 3173)
Strausberg,R.
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                                                                                  /tissue_type="melanoma (McMc cell line)"
/clene_lib="762 (synonym: hmel2). Vector psportl, host
DH10B: sites NotI + salI"
/dev_stage="adult"
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IMAGE:2959399, mkNA, complete cds.
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cDNA Library Arrayed by: The LLMLA.S.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/profein_id="CAB82418.1"
/db_xrof="G1:7*28175"
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/orqanism-"Homo sapiens"
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                /db_xret-"taxon:9606"
                                         /map="6q22-q27"
/clone="DKFXp762H157"
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                       /codon_start-2
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Clone distribution: MGC clone distribution information can be found
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REKROMMREKEFILMI.RLODYEFYTKRAFPELSEQIOPALQLEEFPRRAGEGAEPLEAD
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RDDRNEFKRTTEAFKNERVQRQLLTLSSFLSQARDFNKRTHNDTTHNFNMRQGRDKYK
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Human DNA sequence from clone RPI1-503010 on chromosome 6425.2 26,
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                                                                                                                                                                                   through the I.M.A.G E Consortion/LLNL at: http://image.llnl.gov
Series: HAL Plate: 2 Row: a Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9257254.
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
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Eskarjota, Metamoa, Chordata, Craniata, Vertebrata; Enfeleostomi;
Mammalia; Butheria; Primates, Catarrhini; Hominidae, Homo.
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On Sep 12, 2001 this sequence version replaced qi:14586238.
During sequence assembly data is compared from overlapping clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"Similar to villin 2 (ezrin)"
                                                                                                                                                                                                                                                                                                                                         /Organism_Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:1584 IMAGE:2959:999"
/tissue_type="Colon, adenocarcinoma"
/lab_host="DHIOB-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                         Greene, Mark Ketteman and Anuradha Madan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id-"AAH13903.1"
/db_xref'"GI:15530243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-856-070-23 (1-11) x BC013903 (1-3173)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /acte-"Vector: pOTB7"
142. .1902
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AL589931 AC023785
AL589931.14 GI:15591370
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Sehra, H.
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100.00%
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Best Local Similarity:
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PUBMED
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                together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate remissing or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats. All regions were covered by at least assembly was confirmed by restriction dignst the following
                                                                                                                                                                                                                                                                 abbreviátions are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL, SW., SWISSPOT: Ir. TREMEL, Wp., WORMPEP, Information on the WOPMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear PRI 19-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 6, constincted by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ll-507010 is from the library RPCI-11 2 constructed by the group
Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordala, Craniala, Vertebrata, Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
Fadici, A., Chen, X.C. and Naftolin, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156422. .156454
/note-"Sequence from uni-directional primer reads only."
                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.a- a_k/P_{\rm LG}/-e_{\rm LG}erlegans/weinger This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RPI1-507C10 The true right end of clone PPI1-114M11 is at 47323 in this sequence. Location/Qualitiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Znote~"Single clone region. Sequence from reads from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    short insert library derived from a single pUC clone. Restriction digest data \exp(i\pi \pi) the assembly "
Where differences are found these are annotated as variations
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Mismatches:
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AF189213
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/HGP/Chr6
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/clone_11b="FPG1-11.2"
37002, .37057
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A gene family consisting of earin, radixin and mossin. Its specific localization at actin filament/plasma membrane association situs 93055012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="TGMYGINYFEIKNKKGIDLWLGVDALGINIYEKDDKLAPKIGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSETPNISFNDKKFVIKFIDKKAPDEVFYAFRLFTNKFILQLOM:NHFLYMPPRKDT
IEVQQMKAQAREEKXQNQLERQOLETEKKPPEXVEPEKFQMMPEKEELMLRLQDYED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MINNA Linear ROD 13-AUG-1996
Unpublished
2 (bases 1 to 478)
Fadiel, A., Chen, Z.C. and Naftolin, F.
Direct. Submission
Sobmitted (23-SEP-1999) CB/GYN, Yale University, 333 Cedar Street, New Haven, Ct. 06520, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Motazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae; Murinae; Mus.
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Sato, N., Fundyama, N., Nagafuchi, A., Yomemura, S., Isakita, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Funayama,N., Nagafuchi,A., Sato,N., Tsukita,S. and Tsukita,S. Radkakin is a novel member of the band 4.1 lamily 92.064635 (4), 1039-1048 (1991)
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Physiological Sciences, Myodibil Okaraki 144, JAPAN
2 (bases 1 to 2701)
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/ccil_type="leukemia cells"
/1...478
/noie="villin 2; kinase substrate"
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/db_xref="G1:6063147"
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                                                                                                                                                                                             /organism-"Homo sapiens"
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/chromosome-"6"
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FLQVKIGTILSGETYCPPETAVILGSYAVQAKFGPYNKEMIIKSGYLSSFFLTDQFVMM
IIKI SIOQWEDPTQVWIRAHPGMLKDSAMLFYLKTAQDLEMYGTINYFEIKNKKGTDLWL
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RAMALKAKERIERGAGIOJRSGEOLAAELAEYTAKLALLEBARRRKEDEVERWÜRAK

EAGNOLVKTKEELHLVMTRPPPPPPPPYEPVNYHVOEGLODEGAEPMGYSAELSSEGI

LDÖRNEEKTTTARKENTPVORGLIJTLSNELSGAPPENKRTHNDITHNENMPGSPDKYY

TEROTROKTORTEGAM.
                                                                                                                                                                                                              /db_xref="SWISS_PROF;P26040"
/fraesiafion="MBKPINVBVTIMOAREBAIQDNPTCRQLEDQVVKTIGLEBVWY
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Mus musculus chromosome 16 clone PP23-3512, WOPKING DPAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                 GVDALGLNIYEKITEKLIFKI GEPWSE I RNI SENDKKEV I KETDKKAPDEVEYALFRIKL
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Mammalia; Eutheria; Bodentia, Sciatograthi; Mazidae; Muzinae; Mus.
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/db_xrel-"taxon.10090"
/cell_line-"F9"
/clonc_lib-"lambda_gtll"
                                                                                                                     /product-"ezrin"
/protein_id="CAA44086.1"
/db_xret-"GI:50881"
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 16
                                                                                                                                                                                        /db_xref-"MGD:MGL:98931"
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Center: Joint Genome Institute
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DOE Joint Genome Institute.
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Estimated insert size: 160802; sum-of-configs estimation Quality coverage: 3.02 in Q20 bases; agarose-tp estimation Quality coverage: 3.34 in Q20 bases; sum-of-configs estimation.

* NOTE: Phis is a 'working draft' sequence. It currently
* consists of 26 configs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                           * as soon as it is available and the accession number will be preserved.
                                                                                     * arbitrary. Gaps between the contids are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
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contig of 41175 bp in length
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contig of 1151 bp in length
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Pred. No.: 9.18 Length: 183302 Score: 52.00 Matches: 10 Dercent Similarity: 100.00% Conservative: 1 Obs. Ob	5	AUTHORS Han, J. Montgomerry, T., Grills, G., Icc. E., Long, J., Pomerantz, R., AUTHORS Han, J., Montgomerry, T., Crills, G., Icc. E., Long, J., Pomerantz, R., Lorden, E., Shim, C., Docker, J., Thomas, F., Porera, A., Lorden, E., High Throughput Mouse Sequencing JOURNAL Unpublished FEFFERNF 2 (bases 1 to 207782) FORTHORS Han, J., Montgomerry, K.T., Grills, C., Ire, F., Long, I., Powerantz, P., Loshikhes, I. P., Shim, C., Docker, J., Thomas, E., Pereta, A., Loshikhes, I. P., Shim, C., Docker, J., Thomas, E., Pereta, A., Loshikhes, I. P., Shim, C., Docker, J., Thomas, E., Dereta, A., Loshikhes, I. P., Shim, C., Docker, J., Thomas, E., Dereta, A., Loshikhes, I. P., Shim, C., Docker, J., Thomas, E., Dereta, A., Loshikhes, I. P., Shim, C., Docker, J., Thomas, E., Dereta, A., Lishikhes, I. Shim, C., Docker, J., Thomas, E., Johnson, A., Loshikhes, I. Shim, College of Medicine Genome Center, 1300 Morris Park Ave, Leone, Av., 1966	Einstein College of Medicine Genome Center, 1300 Morris Probas 1 (bases) 1 (2072) Bunday 10441, 183 (bases) 1 (2072) Inshikhes, LP and Kucherlapati, P. Direct Submission Schmitted (14 DEC 2001) Hardud Furthurs Center for Genomics, Harvard Medical School, 65 Landsdowne St., Cambo 02139, USA On Oct 20, 2000 this Sequence version replaced gi:10799316 Center: Harvard Parliers Genome Center Center Center: Harvard Parliers Genome Center Center Contest: Harvard Parliers Genome Center Center Code: HDGC Web site, http://www.hpsyg.phySc.pu.nocymens.html. Contact: Haggemendel.mgh.harvard.cdu Contact: Haggemendel.mgh.harvard.cdu Contact: Hoperen Perls: LASS processes Processes Genomers Genter Project name: AED Sequencing vector: Profit 177266 at least Q20 *Consensus quality: 186969 at least Q30 *Consensus quality: 186969 at least of the appeared at last no working draft, Sequence record is ablitrary. Gaps between the contigs are represented as rous of N, but the exact sizes of the appeared at last no working of Hiss sequence record is a soun as it is available and the accession number Will be preserved. * Barbitrary Gaps between the contigs are represented as Soun as it is available and the accession number Will be preserved.

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Submitted (91 FEB 2000) Department of Molecular Genetics, Albert
Einstein College of Medicine Genome Center, 1900 Morris Park Ave.,
Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                              quality coverage. against FF - N/A quality coverage: 8.5 x in Q20 bases; sum of-configs estimation
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                                                            On Jan 4, 2002 this sequence version replaced qi:11094413.
                                                                                                                                                                                                                                                                                                                                                                                     * NOTE. This is a 'working draft' sequence. It currently consists of 11 contids. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                     * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                gap of unknown length conting of 3885 bp in length gap of unknown length ecnting of 28075 bp in length gap of unknown length
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215751. gap of unknown length
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216675: contig of 855 bp in length
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217917; contiq of 1222 bp in 1
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Chemistry: Dye terminator Biq Dye, 100%
*Consensus quality: 212564 at least 020
*Consensus quality: 21720 at least 040
*Consensus quality: 210739 at least 040
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/strain="C57BL6/J"
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/clone="RP23-103120"
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Montgomery,K.T., Grills,G., Han,J., Lee,E., Long,J., Pemerantz,E.,
Loshikhes,I.P., Shim,P., Invekey,J., Thomas,F., Perera,A.,
Gordon,M., Golls,J.S. and Kucherlapati,R.
Direct Submission.
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205727: qap of unknown length
207782: contig of 2055 bp in length.
 190625: contiq of 2715 bp in length
190645. gap of unknown length
192088: contig of 1443 bp in length
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is not known and their order in this sequence record is

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ORIGIN
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Parkway, St. Louis, MC 63108, OSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metaboa, Chorlula, Craniata, Vortolina, Eutoloostomi,
Mammalia: Euthoria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus chromosomo UNK clone PP24-342H13, WoPFING DPAFT SOFENCE, 10 unordered pieces.
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Ouality coverage: 8.54 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: plasmid: 100% Chemistry: Dye-primer ET: 0% of reads Chemistry: Dye-primer ET: 0% of reads Chemistry: Dye-primer ET: 0% of reads Assembly program: physics of 940000 Consensus quality: 283924 bases at least 040 Consensus quality: 283778 bases at least 030 Consensus quality: 286926 bases at least 020 Insert size: 225900, agaicserify Insert size: 304647; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site.http://gehome.wusfl.edu/gsc/index_shtml
                                                                                                                /note-"assembly_name.Contig204"
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215921 216675
              /note-"assembly_name:Contig205"
214253, .215731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 10729 GAGPTGATGPTTPGGTTGTAGGATAPGAGPA; 10697
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HTG; HTGS_PHASE1; HTGS_DRAFT.
209273. .214332
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linear PRI 19-0CT-1999
* arbitrary, Gaps between the contias are represented as * tuns of N, but the exact sizes of the gaps are unknown. This record Will be updated With the finished sequence * as seen as it is available and the accession number Will * be preserved.
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160857: gap of unknown length
284417: contig of 123560 bp in length
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gap of unknown length
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285468: gap of unknown length
286508: contig of 1040 bp in length.
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Direct Submission
Submitted (22 SEP 1999) OB/GYN, Yale University, 333 Cedar Street,
New Haven, CT 06511, USA
                                          Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Pokaryota: Metazoa; Chordata; Craniata Homo, Homo,
                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/map-figi2-q27
/cell_line-"Bix3"
/rell_type-"epithelial cancer cells"
/tissuc_type-"ovary"
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Mismatches:
                                                                                1 (bases I to 475)
Chen, Z.C., Fadiel, A. and Naftolin, F.
Ezrin gene mutation in ovarian cancer Inpublished
2 (bases I to 475)
Chen, Z.C., Fadiel, A. and Naftolin, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
                                                                                                                                                                                                                Location/Qualifiers
1. 475
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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/product-"ezrin"
AF188897.1 G1:6063144
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90.91%
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                            Homo sapiens.
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Best Local Similarity:
Ouery Match:
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                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                   REFERENCE
AUTHORS
TITLE
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                                                                                                                             JOURNAL REFERENCE
            KEYWORDS
SOURCE
                                                                                                                                                                                       JOSH WALL
                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                               SIL
                                                                                                                                                                                                                FEATURES
VERSTON
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Search completed: January 16, 2003, 19:05:54 Job time : 1034.47 secs

1 GluLeuMetLeuArgLeuGlnAspTyrGlu 10

US 09-856-070-23 (1 11) x AF188897 (1-475)